



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 07:59 PM UTC

PDB ID : 5HCC / pdb_00005hcc
Title : Ternary complex of human Complement C5 with Ornithodoros moubata OmCI and Dermacentor andersoni RaCI3.
Authors : Jore, M.M.; Johnson, S.; Lea, S.M.
Deposited on : 2016-01-04
Resolution : 2.59 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

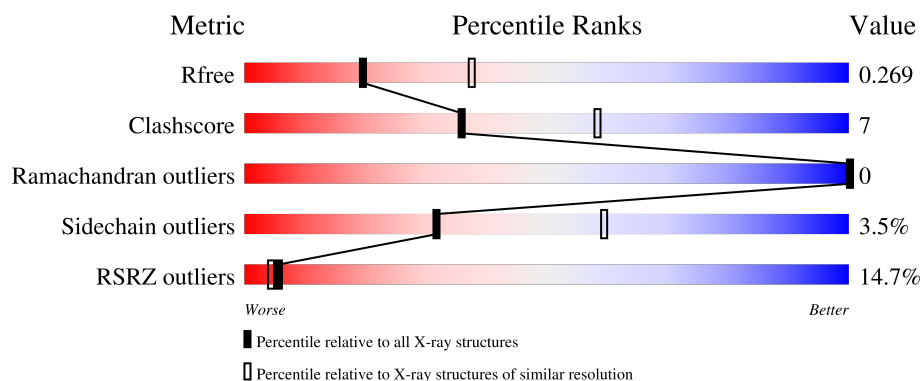
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	656	15% 77% 21% ..
2	A	998	16% 78% 19% ..
3	C	165	5% 80% 9% 10%
4	D	81	5% 46% 10% 42%
5	E	2	100%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 14646 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Complement C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	647	Total	C	N	O	S	0	0	0
			5116	3281	819	1003	13			

- Molecule 2 is a protein called Complement C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	982	Total	C	N	O	S	0	0	0
			7776	4973	1298	1464	41			

- Molecule 3 is a protein called Complement inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	148	Total	C	N	O	S	0	0	0
			1160	715	195	239	11			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	4	MET	-	initiating methionine	UNP Q5YD59
C	5	ALA	-	expression tag	UNP Q5YD59
C	6	SER	-	expression tag	UNP Q5YD59
C	7	HIS	-	expression tag	UNP Q5YD59
C	8	HIS	-	expression tag	UNP Q5YD59
C	9	HIS	-	expression tag	UNP Q5YD59
C	10	HIS	-	expression tag	UNP Q5YD59
C	11	HIS	-	expression tag	UNP Q5YD59
C	12	HIS	-	expression tag	UNP Q5YD59
C	13	HIS	-	expression tag	UNP Q5YD59
C	14	HIS	-	expression tag	UNP Q5YD59
C	15	HIS	-	expression tag	UNP Q5YD59
C	16	HIS	-	expression tag	UNP Q5YD59
C	17	SER	-	expression tag	UNP Q5YD59

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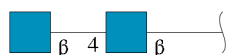
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Chain	Residue	Modelled	Actual	Comment	Reference
C	18	GLY	-	expression tag	UNP Q5YD59
C	78	GLN	ASN	engineered mutation	UNP Q5YD59
C	102	GLN	ASN	engineered mutation	UNP Q5YD59

- Molecule 4 is a protein called Dermacentor andersoni RaCI3.

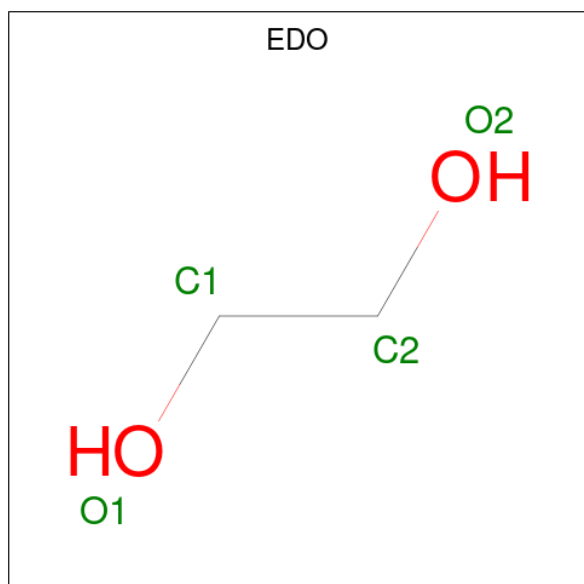
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	47	Total	C	N	O	S	0	0	0
			351	210	65	69	7			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



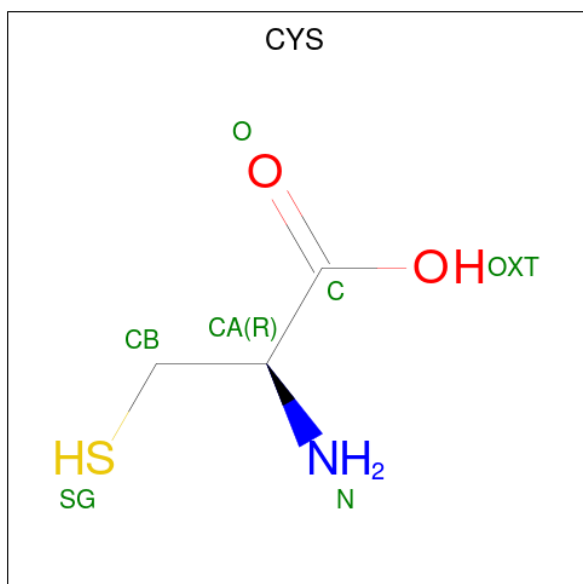
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		

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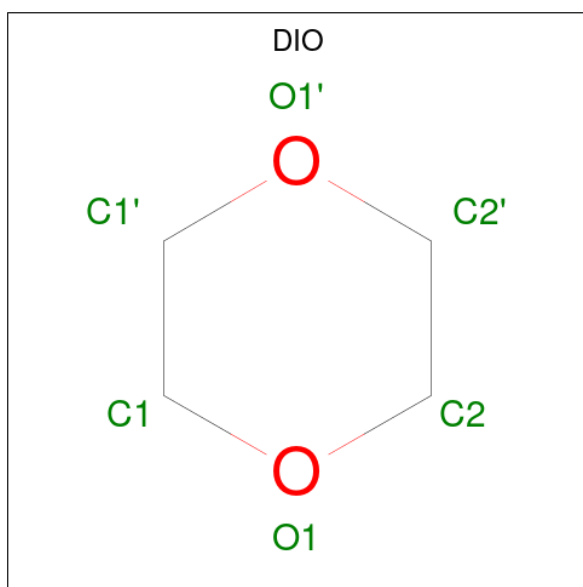
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is CYSTEINE (CCD ID: CYS) (formula: $C_3H_7NO_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	S	0	0
			6	3	1	1	1		

- Molecule 8 is 1,4-DIETHYLENE DIOXIDE (CCD ID: DIO) (formula: $C_4H_8O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	4	2		

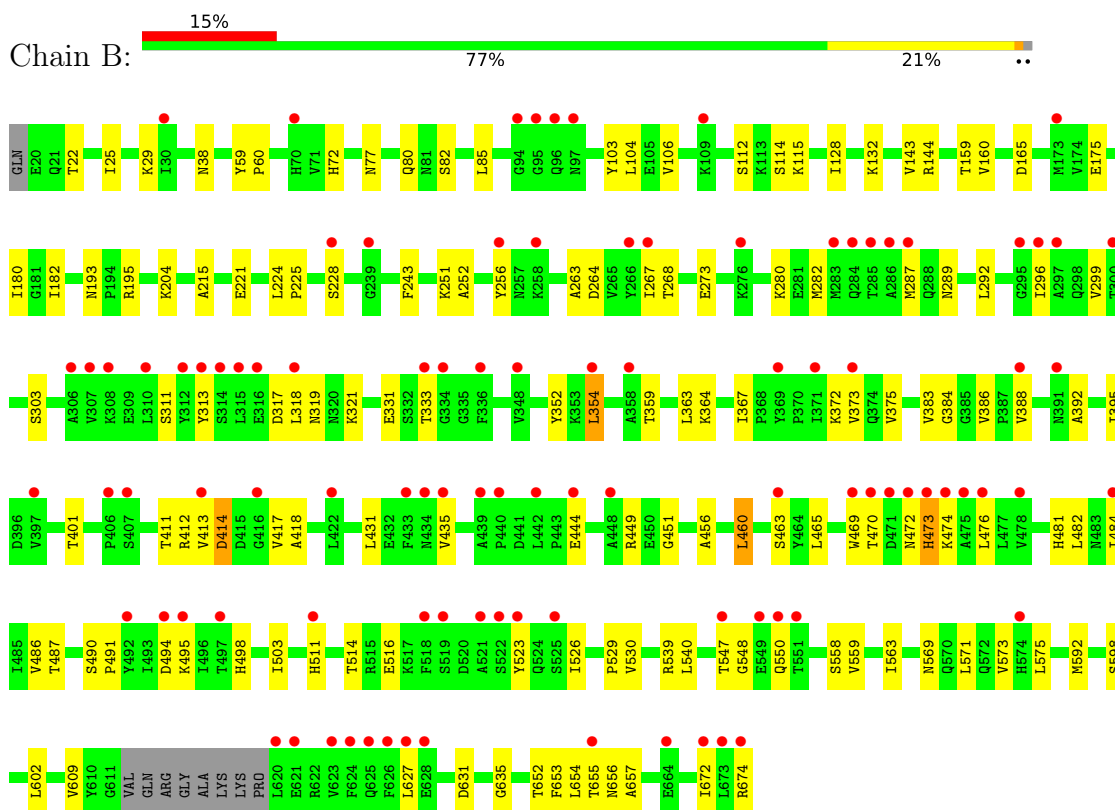
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	62	Total	O	0	0
			62	62		
9	A	105	Total	O	0	0
			105	105		
9	C	3	Total	O	0	0
			3	3		
9	D	5	Total	O	0	0
			5	5		

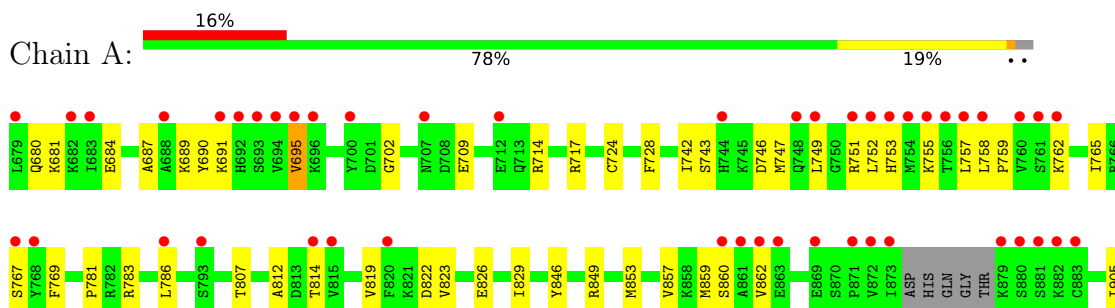
3 Residue-property plots [i](#)

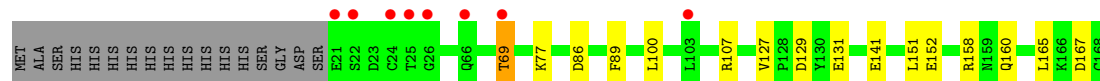
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Complement C5

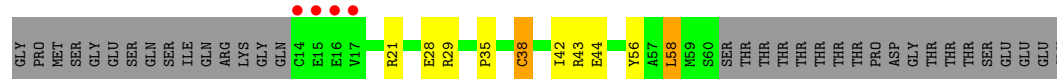


• Molecule 2: Complement C5





Chain D:



Chain E: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.87Å 140.28Å 211.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.57 – 2.59 66.57 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.2 (66.57-2.59) 99.4 (66.57-2.59)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.58Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.231 , 0.267 0.233 , 0.269	Depositor DCC
R_{free} test set	4841 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14646	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NAG, DIO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.15	0/5234	0.35	0/7119
2	A	0.18	0/7933	0.39	2/10740 (0.0%)
3	C	0.13	0/1183	0.30	0/1599
4	D	0.16	0/355	0.37	0/480
All	All	0.16	0/14705	0.37	2/19938 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1515	LYS	N-CA-C	-7.99	96.84	109.23
2	A	1655	SER	CB-CA-C	-6.33	108.62	117.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5116	0	5022	84	0
2	A	7776	0	7822	121	0
3	C	1160	0	1085	8	0
4	D	351	0	332	6	0
5	E	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	12	0	18	3	0
6	B	8	0	12	0	0
6	C	4	0	6	0	0
6	D	4	0	6	0	0
7	A	6	0	3	0	0
8	A	6	0	8	3	0
9	A	105	0	0	2	0
9	B	62	0	0	1	0
9	C	3	0	0	0	0
9	D	5	0	0	0	0
All	All	14646	0	14339	211	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (211) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1515:LYS:HG2	2:A:1516:ILE:HA	1.61	0.82
2:A:1515:LYS:HE3	2:A:1516:ILE:HG23	1.60	0.81
1:B:373:VAL:HG21	1:B:388:VAL:HG11	1.64	0.78
1:B:469:TRP:HA	1:B:484:ILE:HA	1.67	0.77
3:C:77:LYS:NZ	3:C:167:ASP:O	2.22	0.72
1:B:359:THR:HG21	1:B:372:LYS:H	1.55	0.71
2:A:1576:LYS:HE2	2:A:1601:ILE:HD11	1.73	0.71
2:A:942:VAL:HG21	2:A:957:LYS:HG2	1.72	0.71
2:A:1625:LEU:HB2	2:A:1636:ILE:HG23	1.72	0.70
2:A:1556:GLU:HB3	2:A:1622:LYS:HE2	1.73	0.69
1:B:384:GLY:HA3	1:B:413:VAL:HG23	1.75	0.68
1:B:487:THR:HG22	1:B:523:TYR:HB3	1.75	0.68
1:B:268:THR:HG22	1:B:287:MET:HG2	1.75	0.67
1:B:655:THR:HG22	1:B:657:ALA:H	1.58	0.66
2:A:751:ARG:O	2:A:755:LYS:HB2	1.96	0.65
2:A:1517:GLN:NE2	2:A:1604:VAL:O	2.27	0.65
1:B:251:LYS:HG2	1:B:296:ILE:HG12	1.78	0.65
2:A:695:VAL:HG21	2:A:724:CYS:HA	1.77	0.65
3:C:107:ARG:NH1	3:C:131:GLU:OE1	2.30	0.64
2:A:1612:VAL:HB	2:A:1615:ARG:HD2	1.80	0.64
2:A:1226:ARG:NH1	3:C:141:GLU:OE1	2.31	0.63
2:A:1532:CYS:HA	2:A:1640:ASP:HA	1.78	0.63
2:A:859:MET:HE2	2:A:910:ILE:HG21	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:979:VAL:HG12	2:A:1328:MET:HE1	1.81	0.63
1:B:193:ASN:O	2:A:1058:SER:OG	2.14	0.62
2:A:975:ARG:NH2	2:A:1344:ASP:O	2.31	0.62
2:A:1370:THR:HG21	2:A:1506:THR:HB	1.80	0.62
1:B:25:ILE:O	1:B:653:PHE:HA	1.98	0.62
2:A:1060:ARG:NH1	6:A:2003:EDO:O1	2.31	0.62
1:B:72:HIS:O	1:B:77:ASN:ND2	2.34	0.60
2:A:1432:ILE:HG13	2:A:1511:THR:HG21	1.83	0.60
1:B:386:VAL:H	1:B:411:THR:HB	1.67	0.60
2:A:743:SER:OG	2:A:746:ASP:OD1	2.20	0.59
2:A:934:VAL:HG23	2:A:1508:PHE:CZ	2.38	0.59
2:A:905:ILE:HD13	2:A:931:PRO:HG3	1.85	0.58
2:A:749:LEU:HD23	2:A:752:LEU:HD12	1.86	0.57
2:A:1154:LYS:NZ	8:A:2007:DIO:H12	2.19	0.57
2:A:857:VAL:HA	2:A:913:SER:O	2.03	0.57
3:C:129:ASP:OD1	3:C:158:ARG:NH2	2.37	0.57
2:A:1544:SER:O	2:A:1546:GLU:N	2.33	0.57
1:B:569:ASN:ND2	1:B:598:SER:HB2	2.20	0.56
2:A:1622:LYS:HE3	2:A:1642:LEU:HD23	1.86	0.56
1:B:414:ASP:OD1	1:B:414:ASP:N	2.39	0.56
1:B:444:GLU:O	1:B:449:ARG:NH2	2.39	0.56
2:A:977:LEU:HD21	2:A:1315:VAL:HG11	1.89	0.55
1:B:38:ASN:ND2	1:B:82:SER:OG	2.31	0.55
1:B:104:LEU:O	1:B:114:SER:HA	2.07	0.55
1:B:503:ILE:HB	1:B:511:HIS:HB2	1.89	0.55
1:B:592:MET:HE2	2:A:786:LEU:HD22	1.89	0.55
1:B:165:ASP:OD2	1:B:195:ARG:NH1	2.36	0.54
1:B:132:LYS:HD2	1:B:609:VAL:HG11	1.88	0.54
2:A:934:VAL:HG22	2:A:1492:THR:HG21	1.89	0.54
2:A:1012:LEU:HD21	2:A:1056:ILE:HD12	1.90	0.54
2:A:1129:LEU:HD13	2:A:1139:GLU:HB3	1.89	0.54
2:A:1154:LYS:HZ3	8:A:2007:DIO:H12	1.73	0.54
2:A:1320:LYS:HG2	2:A:1342:LEU:HD13	1.88	0.53
1:B:204:LYS:NZ	4:D:28:GLU:OE1	2.33	0.53
1:B:38:ASN:HD21	1:B:82:SER:HG	1.53	0.53
2:A:1548:ARG:HH11	2:A:1644:TRP:HH2	1.57	0.53
2:A:822:ASP:HB2	2:A:849:ARG:HG3	1.90	0.53
1:B:22:THR:HA	1:B:656:ASN:HD21	1.73	0.53
2:A:823:VAL:HA	2:A:846:TYR:O	2.09	0.53
4:D:21:ARG:HD3	4:D:29:ARG:HE	1.74	0.53
2:A:1219:LYS:HB2	2:A:1225:TYR:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:412:ARG:N	1:B:417:VAL:O	2.35	0.52
2:A:1516:ILE:HG22	2:A:1517:GLN:H	1.75	0.52
2:A:923:LEU:HD11	2:A:925:LYS:HZ2	1.75	0.52
2:A:1315:VAL:HG12	2:A:1348:VAL:HG22	1.92	0.52
1:B:273:GLU:OE2	1:B:321:LYS:NZ	2.43	0.51
2:A:1066:TYR:HB3	2:A:1078:LEU:HD23	1.91	0.51
2:A:1548:ARG:NH1	2:A:1646:GLU:OE1	2.43	0.51
1:B:463:SER:HA	1:B:490:SER:HB2	1.93	0.51
1:B:469:TRP:HZ3	1:B:559:VAL:HB	1.75	0.51
2:A:1095:GLN:OE1	6:A:2005:EDO:O1	2.28	0.51
1:B:352:TYR:HE1	1:B:383:VAL:HG11	1.76	0.50
1:B:364:LYS:HB3	1:B:367:ILE:HD13	1.93	0.50
2:A:1187:THR:HA	2:A:1190:ILE:HG22	1.91	0.50
2:A:1290:THR:O	2:A:1294:ILE:HG12	2.10	0.50
1:B:476:LEU:HB2	1:B:563:ILE:HG12	1.94	0.50
2:A:969:PRO:HG3	2:A:1601:ILE:HG21	1.94	0.50
2:A:975:ARG:HA	2:A:1362:THR:O	2.12	0.50
1:B:417:VAL:HG21	1:B:473:HIS:CD2	2.47	0.50
1:B:547:THR:OG1	1:B:548:GLY:N	2.45	0.50
1:B:573:VAL:HG12	1:B:592:MET:HG2	1.94	0.50
2:A:1324:HIS:HE1	2:A:1338:VAL:HG11	1.76	0.50
1:B:80:GLN:NE2	1:B:514:THR:OG1	2.45	0.50
1:B:451:GLY:O	1:B:674:ARG:NH2	2.45	0.49
1:B:395:ILE:HG12	1:B:401:THR:HG22	1.94	0.49
2:A:1019:PHE:CZ	2:A:1088:GLN:HB3	2.46	0.49
1:B:263:ALA:HB3	1:B:292:LEU:HB3	1.94	0.49
2:A:987:ILE:HD13	2:A:1294:ILE:HG23	1.94	0.49
1:B:503:ILE:HG12	1:B:540:LEU:HD13	1.93	0.49
2:A:1013:MET:HE3	2:A:1287:THR:HB	1.94	0.49
2:A:942:VAL:CG2	2:A:957:LYS:HG2	2.40	0.49
2:A:1618:LEU:O	2:A:1645:ILE:HA	2.13	0.49
1:B:539:ARG:NH2	1:B:635:GLY:O	2.46	0.49
1:B:469:TRP:CD1	1:B:482:LEU:HD11	2.48	0.49
1:B:498:HIS:CE1	1:B:516:GLU:HG2	2.48	0.49
1:B:29:LYS:HD2	1:B:652:THR:HG23	1.95	0.48
2:A:714:ARG:HA	2:A:717:ARG:HH21	1.78	0.48
3:C:152:GLU:HG2	3:C:160:GLN:HE22	1.78	0.48
1:B:221:GLU:OE1	2:A:762:LYS:NZ	2.44	0.48
2:A:1598:ILE:HD12	2:A:1637:TYR:HE1	1.77	0.48
2:A:1567:SER:HB2	2:A:1578:LYS:HD2	1.94	0.48
2:A:1450:PHE:CZ	2:A:1475:VAL:HB	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1316:SER:HA	2:A:1323:LEU:H	1.78	0.48
2:A:1031:TRP:HB3	2:A:1038:PRO:HB3	1.95	0.48
2:A:1576:LYS:HG2	2:A:1601:ILE:HG12	1.96	0.47
1:B:359:THR:HG21	1:B:372:LYS:N	2.26	0.47
2:A:1535:MET:HG3	2:A:1645:ILE:HD11	1.96	0.47
2:A:681:LYS:HA	2:A:684:GLU:HB2	1.96	0.47
2:A:829:ILE:HG13	2:A:925:LYS:HG2	1.96	0.47
1:B:318:LEU:HA	1:B:321:LYS:HG3	1.96	0.47
2:A:981:GLY:HA3	2:A:1333:PHE:HB2	1.96	0.47
2:A:915:GLU:HG2	2:A:920:LYS:HG3	1.95	0.47
2:A:1108:VAL:HG21	2:A:1164:ILE:HG22	1.97	0.47
2:A:1235:LYS:NZ	2:A:1413:GLU:OE1	2.45	0.47
2:A:1222:PRO:HG2	3:C:165:LEU:HD11	1.97	0.47
2:A:1652:THR:HG22	2:A:1658:GLN:HB2	1.97	0.47
2:A:823:VAL:HG21	2:A:853:MET:SD	2.55	0.47
1:B:180:ILE:HG13	1:B:182:ILE:H	1.79	0.46
2:A:1032:ASN:OD1	2:A:1032:ASN:N	2.48	0.46
1:B:25:ILE:HB	1:B:654:LEU:HB2	1.97	0.46
1:B:160:VAL:HG22	1:B:175:GLU:HB3	1.96	0.46
2:A:751:ARG:O	2:A:755:LYS:CB	2.63	0.46
1:B:331:GLU:OE2	1:B:333:THR:OG1	2.27	0.46
1:B:383:VAL:O	1:B:411:THR:HG21	2.15	0.46
1:B:571:LEU:HG	2:A:812:ALA:HB2	1.98	0.46
2:A:984:VAL:HG23	2:A:987:ILE:HD12	1.98	0.46
4:D:42:ILE:HG22	4:D:44:GLU:H	1.80	0.46
2:A:781:PRO:C	2:A:783:ARG:H	2.24	0.46
1:B:317:ASP:C	1:B:319:ASN:H	2.24	0.46
1:B:540:LEU:O	1:B:558:SER:HA	2.16	0.45
1:B:59:TYR:HA	1:B:60:PRO:HA	1.79	0.45
1:B:354:LEU:HD23	1:B:435:VAL:HG23	1.97	0.45
1:B:115:LYS:HB2	1:B:654:LEU:HD21	1.97	0.45
2:A:937:GLU:HG3	2:A:1364:VAL:HG22	1.96	0.45
2:A:1565:ILE:HD11	2:A:1611:LEU:HD13	1.98	0.45
1:B:373:VAL:HG22	1:B:418:ALA:HB3	1.98	0.45
1:B:469:TRP:CD1	1:B:469:TRP:O	2.70	0.45
2:A:1318:LYS:HE3	2:A:1319:HIS:CE1	2.52	0.45
1:B:29:LYS:HA	1:B:652:THR:HG23	1.99	0.45
1:B:144:ARG:NH2	1:B:602:LEU:O	2.46	0.45
1:B:490:SER:OG	1:B:491:PRO:O	2.17	0.45
2:A:1088:GLN:HG2	8:A:2007:DIO:H1'2	1.98	0.44
1:B:417:VAL:HG21	1:B:473:HIS:NE2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:465:LEU:HD11	1:B:486:VAL:HG13	1.98	0.44
1:B:280:LYS:HE2	1:B:282:MET:HE2	1.99	0.44
1:B:311:SER:O	1:B:313:TYR:N	2.51	0.44
2:A:1554:LYS:HG3	2:A:1556:GLU:H	1.82	0.44
2:A:1402:ILE:HG13	2:A:1479:ILE:HD13	1.99	0.44
4:D:58:LEU:HD12	4:D:58:LEU:HA	1.82	0.44
2:A:687:ALA:O	2:A:691:LYS:HG3	2.18	0.43
2:A:765:ILE:HG13	2:A:767:SER:H	1.84	0.43
2:A:860:SER:HB3	2:A:911:ASN:H	1.83	0.43
2:A:1008:ALA:HB2	2:A:1059:TYR:CG	2.54	0.43
2:A:1464:LEU:HD23	2:A:1467:ILE:HG12	1.99	0.43
1:B:363:LEU:HB2	1:B:456:ALA:HA	2.00	0.43
2:A:1386:ILE:HD12	2:A:1386:ILE:HA	1.86	0.43
1:B:243:PHE:O	1:B:303:SER:HB2	2.19	0.43
2:A:905:ILE:HG21	2:A:931:PRO:HG3	2.00	0.43
2:A:1279:ARG:HD2	9:A:2137:HOH:O	2.19	0.43
1:B:392:ALA:HB1	1:B:431:LEU:HD11	2.01	0.43
2:A:826:GLU:HG2	2:A:846:TYR:HE1	1.84	0.43
2:A:1046:LYS:NZ	2:A:1092:TYR:O	2.52	0.43
3:C:69:THR:HA	3:C:89:PHE:O	2.19	0.43
1:B:106:VAL:O	1:B:112:SER:HA	2.18	0.43
2:A:1645:ILE:O	2:A:1645:ILE:HG13	2.17	0.43
2:A:758:LEU:HB2	2:A:759:PRO:HD3	2.01	0.42
2:A:1516:ILE:CG2	2:A:1518:LYS:HG2	2.49	0.42
2:A:859:MET:HE3	2:A:912:PHE:CE1	2.54	0.42
9:B:849:HOH:O	6:A:2005:EDO:H11	2.18	0.42
2:A:1516:ILE:HG22	2:A:1517:GLN:N	2.34	0.42
1:B:228:SER:O	1:B:252:ALA:HA	2.19	0.42
2:A:1232:LEU:HB2	2:A:1235:LYS:HD3	2.02	0.42
2:A:680:GLN:HG3	2:A:753:HIS:NE2	2.35	0.42
2:A:709:GLU:OE1	2:A:717:ARG:NH2	2.52	0.42
1:B:609:VAL:HG12	2:A:769:PHE:CG	2.55	0.42
2:A:691:LYS:HE2	2:A:757:LEU:HD13	2.02	0.42
2:A:964:PRO:HG2	2:A:967:LEU:HB2	2.01	0.42
2:A:999:ILE:HG13	2:A:1000:LEU:HG	2.01	0.42
3:C:86:ASP:O	3:C:100:LEU:HD13	2.20	0.41
1:B:159:THR:O	1:B:175:GLU:HA	2.20	0.41
1:B:224:LEU:HD12	1:B:225:PRO:HD2	2.01	0.41
1:B:539:ARG:NH1	1:B:631:ASP:OD2	2.53	0.41
2:A:702:GLY:HA2	2:A:728:PHE:CE2	2.56	0.41
2:A:1229:LYS:HD2	2:A:1231:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:35:PRO:HG2	4:D:38:CYS:SG	2.61	0.41
1:B:267:ILE:HD13	1:B:299:VAL:HG21	2.02	0.41
2:A:1105:LEU:O	2:A:1109:GLU:HB2	2.20	0.41
2:A:689:LYS:HD3	2:A:690:TYR:CE1	2.55	0.41
2:A:1616:GLN:OE1	2:A:1650:ARG:NH2	2.54	0.41
1:B:375:VAL:HG11	1:B:386:VAL:HG11	2.02	0.41
2:A:1384:GLN:O	2:A:1400:LYS:HA	2.20	0.41
2:A:1563:VAL:HG12	2:A:1581:LEU:HA	2.02	0.41
1:B:481:HIS:CE1	1:B:529:PRO:HB3	2.56	0.41
1:B:484:ILE:HG22	1:B:526:ILE:O	2.21	0.41
2:A:819:VAL:HG21	9:A:2104:HOH:O	2.20	0.41
2:A:1244:THR:OG1	2:A:1247:MET:HE3	2.21	0.41
2:A:1378:TYR:CE2	2:A:1409:LYS:HG2	2.56	0.41
4:D:43:ARG:NH2	4:D:56:TYR:OH	2.49	0.41
1:B:592:MET:SD	1:B:602:LEU:HD11	2.61	0.40
2:A:1379:LEU:HD22	2:A:1493:PHE:CE2	2.55	0.40
1:B:460:LEU:HD12	1:B:460:LEU:HA	1.87	0.40
2:A:1577:TYR:CE1	2:A:1611:LEU:HB2	2.56	0.40
1:B:128:ILE:HB	1:B:215:ALA:HB2	2.03	0.40
1:B:256:TYR:HA	2:A:846:TYR:HE2	1.86	0.40
2:A:1540:ASP:HB3	2:A:1543:ILE:HD13	2.02	0.40
2:A:1098:ASN:O	2:A:1102:ASN:ND2	2.52	0.40
2:A:1515:LYS:CE	2:A:1516:ILE:HG23	2.41	0.40
1:B:575:LEU:HD23	1:B:575:LEU:HA	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	643/656 (98%)	616 (96%)	27 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	976/998 (98%)	925 (95%)	51 (5%)	0	100	100
3	C	146/165 (88%)	138 (94%)	8 (6%)	0	100	100
4	D	45/81 (56%)	44 (98%)	1 (2%)	0	100	100
All	All	1810/1900 (95%)	1723 (95%)	87 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	574/581 (99%)	556 (97%)	18 (3%)	35	63
2	A	872/885 (98%)	838 (96%)	34 (4%)	28	55
3	C	128/143 (90%)	125 (98%)	3 (2%)	44	71
4	D	41/71 (58%)	39 (95%)	2 (5%)	22	47
All	All	1615/1680 (96%)	1558 (96%)	57 (4%)	32	59

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	85	LEU
1	B	103	TYR
1	B	143	VAL
1	B	264	ASP
1	B	289	ASN
1	B	354	LEU
1	B	414	ASP
1	B	460	LEU
1	B	470	THR
1	B	472	ASN
1	B	473	HIS
1	B	474	LYS
1	B	494	ASP

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Mol	Chain	Res	Type
1	B	495	LYS
1	B	530	VAL
1	B	550	GLN
1	B	627	LEU
1	B	672	ILE
2	A	695	VAL
2	A	742	ILE
2	A	747	MET
2	A	807	THR
2	A	814	THR
2	A	862	VAL
2	A	916	THR
2	A	936	ARG
2	A	962	ARG
2	A	987	ILE
2	A	1056	ILE
2	A	1127	ILE
2	A	1247	MET
2	A	1370	THR
2	A	1462	LEU
2	A	1516	ILE
2	A	1519	VAL
2	A	1526	LYS
2	A	1528	VAL
2	A	1546	GLU
2	A	1573	VAL
2	A	1581	LEU
2	A	1582	LEU
2	A	1589	GLU
2	A	1601	ILE
2	A	1603	LYS
2	A	1636	ILE
2	A	1645	ILE
2	A	1650	ARG
2	A	1651	ASP
2	A	1654	CYS
2	A	1657	CYS
2	A	1658	GLN
2	A	1664	LEU
3	C	69	THR
3	C	127	VAL
3	C	151	LEU

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Mol	Chain	Res	Type
4	D	38	CYS
4	D	58	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	38	ASN
1	B	72	HIS
1	B	472	ASN
1	B	532	GLN
1	B	591	ASN
1	B	665	ASN
2	A	680	GLN
2	A	785	GLN
2	A	1319	HIS
2	A	1448	GLN
2	A	1626	GLN
2	A	1674	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	E	1	5,2	14,14,15	0.34	0	17,19,21	0.50	0
5	NAG	E	2	5	14,14,15	0.26	0	17,19,21	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	E	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

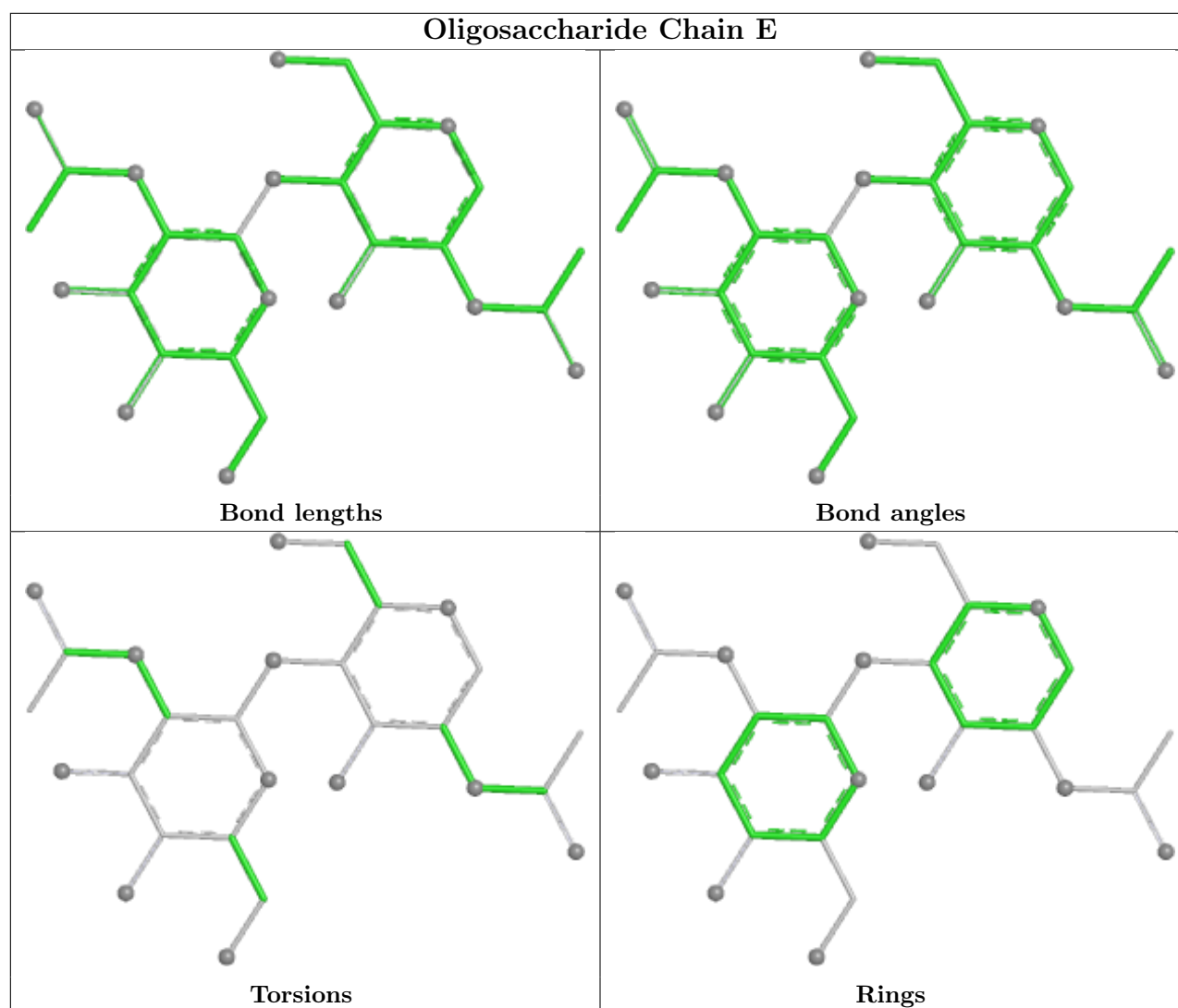
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	EDO	C	201	-	3,3,3	0.44	0	2,2,2	0.29	0
6	EDO	D	101	-	3,3,3	0.44	0	2,2,2	0.33	0
6	EDO	A	2005	-	3,3,3	0.41	0	2,2,2	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	DIO	A	2007	-	6,6,6	0.68	0	6,6,6	0.52	0
6	EDO	A	2003	-	3,3,3	0.35	0	2,2,2	0.61	0
6	EDO	A	2004	-	3,3,3	0.45	0	2,2,2	0.33	0
7	CYS	A	2006	2	4,5,6	0.56	0	1,5,7	0.34	0
6	EDO	B	701	-	3,3,3	0.44	0	2,2,2	0.24	0
6	EDO	B	702	-	3,3,3	0.45	0	2,2,2	0.19	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	C	201	-	-	0/1/1/1	-
6	EDO	D	101	-	-	0/1/1/1	-
6	EDO	A	2005	-	-	0/1/1/1	-
8	DIO	A	2007	-	-	-	0/1/1/1
6	EDO	A	2003	-	-	1/1/1/1	-
6	EDO	A	2004	-	-	0/1/1/1	-
7	CYS	A	2006	2	-	1/1/4/6	-
6	EDO	B	701	-	-	0/1/1/1	-
6	EDO	B	702	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2006	CYS	N-CA-CB-SG
6	A	2003	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	2005	EDO	2	0
8	A	2007	DIO	3	0
6	A	2003	EDO	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	B	647/656 (98%)	0.91	99 (15%) 5 4	36, 73, 125, 178	0
2	A	982/998 (98%)	0.80	158 (16%) 4 3	32, 61, 138, 213	0
3	C	148/165 (89%)	0.64	8 (5%) 31 26	45, 77, 113, 133	0
4	D	47/81 (58%)	0.74	4 (8%) 16 13	44, 66, 98, 136	0
All	All	1824/1900 (96%)	0.82	269 (14%) 6 4	32, 66, 133, 213	0

All (269) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	873	ILE	8.4
1	B	624	PHE	8.2
2	A	1388	ALA	7.7
1	B	623	VAL	7.2
2	A	1517	GLN	6.5
1	B	95	GLY	6.4
1	B	620	LEU	6.4
2	A	1653	THR	6.3
1	B	518	PHE	6.1
2	A	679	LEU	5.5
2	A	755	LYS	5.2
2	A	872	VAL	5.2
2	A	1591	VAL	5.2
2	A	1514	ILE	5.1
2	A	1519	VAL	5.1
2	A	757	LEU	5.1
2	A	1518	LYS	4.9
2	A	1516	ILE	4.9
2	A	756	THR	4.9
2	A	1642	LEU	4.8
1	B	470	THR	4.7

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Mol	Chain	Res	Type	RSRZ
4	D	14	CYS	4.6
2	A	1652	THR	4.6
2	A	1657	CYS	4.6
2	A	1662	ALA	4.6
1	B	523	TYR	4.6
2	A	1524	ALA	4.6
2	A	997	ILE	4.5
2	A	1651	ASP	4.4
2	A	760	VAL	4.4
2	A	752	LEU	4.4
2	A	694	VAL	4.3
1	B	287	MET	4.2
2	A	1601	ILE	4.2
1	B	315	LEU	4.2
1	B	416	GLY	4.2
2	A	1520	CYS	4.2
2	A	1545	ALA	4.0
2	A	1133	LEU	4.0
2	A	762	LYS	4.0
2	A	1605	THR	3.9
1	B	469	TRP	3.8
2	A	1164	ILE	3.8
2	A	1649	PRO	3.8
2	A	1572	ASN	3.8
2	A	1623	GLU	3.8
2	A	881	SER	3.7
2	A	1386	ILE	3.7
2	A	761	SER	3.7
1	B	94	GLY	3.6
1	B	313	TYR	3.6
1	B	444	GLU	3.6
2	A	1570	VAL	3.6
2	A	1655	SER	3.6
1	B	673	LEU	3.6
1	B	307	VAL	3.5
2	A	1648	TRP	3.5
2	A	1326	TYR	3.5
2	A	1656	SER	3.5
1	B	495	LYS	3.5
1	B	284	GLN	3.4
2	A	1635	TYR	3.4
2	A	793	SER	3.4

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Mol	Chain	Res	Type	RSRZ
2	A	869	GLU	3.4
2	A	1650	ARG	3.4
2	A	1671	ILE	3.4
2	A	880	SER	3.4
2	A	695	VAL	3.3
3	C	21	GLU	3.3
1	B	625	GLN	3.3
2	A	883	CYS	3.3
1	B	310	LEU	3.3
2	A	758	LEU	3.3
1	B	621	GLU	3.3
2	A	1644	TRP	3.3
1	B	511	HIS	3.2
1	B	256	TYR	3.2
1	B	333	THR	3.2
1	B	475	ALA	3.2
1	B	521	ALA	3.2
1	B	522	SER	3.2
1	B	626	PHE	3.2
1	B	391	ASN	3.2
2	A	744	HIS	3.2
2	A	1547	THR	3.2
2	A	1571	GLU	3.1
2	A	1663	ASN	3.1
1	B	373	VAL	3.1
4	D	16	GLU	3.0
2	A	1321	GLY	3.0
1	B	551	THR	3.0
2	A	1324	HIS	3.0
2	A	1673	LEU	3.0
1	B	433	PHE	3.0
1	B	434	ASN	3.0
2	A	1327	LYS	3.0
1	B	472	ASN	3.0
3	C	25	THR	2.9
2	A	751	ARG	2.9
2	A	996	GLY	2.9
2	A	1658	GLN	2.9
2	A	995	GLU	2.9
2	A	882	LYS	2.9
1	B	476	LEU	2.9
1	B	494	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	672	ILE	2.9
2	A	1676	CYS	2.9
2	A	1541	LEU	2.9
1	B	574	HIS	2.9
1	B	258	LYS	2.9
2	A	1523	ALA	2.9
1	B	312	TYR	2.9
2	A	1647	TYR	2.9
2	A	861	ALA	2.8
2	A	1521	GLU	2.8
2	A	1633	PHE	2.8
2	A	1669	GLU	2.8
2	A	1533	GLY	2.8
2	A	692	HIS	2.8
1	B	413	VAL	2.8
2	A	1612	VAL	2.8
2	A	1531	ASP	2.8
2	A	1661	LEU	2.8
2	A	1539	LEU	2.7
2	A	1134	PRO	2.7
4	D	15	GLU	2.7
1	B	109	LYS	2.7
1	B	266	TYR	2.7
2	A	768	TYR	2.7
2	A	753	HIS	2.7
1	B	440	PRO	2.7
2	A	1637	TYR	2.7
2	A	1515	LYS	2.6
2	A	1543	ILE	2.6
2	A	1584	ILE	2.6
2	A	1654	CYS	2.6
1	B	286	ALA	2.6
2	A	1561	TYR	2.6
2	A	1627	ILE	2.6
2	A	1645	ILE	2.6
2	A	1625	LEU	2.6
1	B	285	THR	2.6
2	A	1522	GLY	2.6
2	A	754	MET	2.6
2	A	1544	SER	2.6
1	B	497	THR	2.6
2	A	916	THR	2.6

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Mol	Chain	Res	Type	RSRZ
2	A	1132	THR	2.6
2	A	1559	TYR	2.6
1	B	276	LYS	2.6
2	A	1352	PHE	2.6
1	B	628	GLU	2.6
2	A	748	GLN	2.6
1	B	306	ALA	2.6
2	A	863	GLU	2.5
2	A	1346	LEU	2.5
1	B	314	SER	2.5
2	A	993	SER	2.5
1	B	471	ASP	2.5
1	B	655	THR	2.5
2	A	767	SER	2.5
3	C	69	THR	2.5
1	B	358	ALA	2.5
1	B	30	ILE	2.5
2	A	1033	ILE	2.5
1	B	96	GLN	2.5
1	B	525	SER	2.5
1	B	664	GLU	2.4
2	A	1622	LYS	2.4
2	A	1618	LEU	2.4
2	A	1319	HIS	2.4
1	B	547	THR	2.4
1	B	407	SER	2.4
2	A	871	PRO	2.4
2	A	1675	GLY	2.4
1	B	627	LEU	2.4
2	A	965	LEU	2.4
1	B	473	HIS	2.4
1	B	336	PHE	2.4
1	B	674	ARG	2.4
2	A	1279	ARG	2.4
2	A	1667	PHE	2.4
1	B	97	ASN	2.4
2	A	1589	GLU	2.4
2	A	879	LYS	2.4
2	A	1469	SER	2.4
3	C	22	SER	2.4
2	A	1532	CYS	2.4
1	B	173	MET	2.4

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Mol	Chain	Res	Type	RSRZ
3	C	26	GLY	2.3
1	B	442	LEU	2.3
2	A	963	ILE	2.3
2	A	1323	LEU	2.3
2	A	1513	ASN	2.3
1	B	318	LEU	2.3
4	D	17	VAL	2.3
1	B	316	GLU	2.3
2	A	1560	ALA	2.3
2	A	943	THR	2.3
1	B	519	SER	2.3
2	A	1636	ILE	2.3
1	B	474	LYS	2.3
1	B	397	VAL	2.3
2	A	1620	MET	2.3
1	B	478	VAL	2.3
2	A	862	VAL	2.3
2	A	700	TYR	2.3
2	A	1585	TYR	2.3
3	C	24	CYS	2.3
1	B	308	LYS	2.2
1	B	354	LEU	2.2
1	B	463	SER	2.2
2	A	693	SER	2.2
2	A	1604	VAL	2.2
1	B	439	ALA	2.2
1	B	334	GLY	2.2
2	A	1664	LEU	2.2
3	C	103	LEU	2.2
2	A	860	SER	2.2
2	A	712	GLU	2.2
2	A	820	PHE	2.2
1	B	435	VAL	2.2
1	B	297	ALA	2.2
2	A	688	ALA	2.2
2	A	1592	ALA	2.2
1	B	492	TYR	2.2
2	A	691	LYS	2.2
1	B	348	VAL	2.2
1	B	388	VAL	2.2
2	A	682	LYS	2.2
2	A	696	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
2	A	1568	ILE	2.2
2	A	1567	SER	2.2
1	B	239	GLY	2.1
2	A	786	LEU	2.1
1	B	267	ILE	2.1
1	B	228	SER	2.1
2	A	1628	LYS	2.1
2	A	1575	VAL	2.1
1	B	296	ILE	2.1
1	B	70	HIS	2.1
1	B	550	GLN	2.1
1	B	448	ALA	2.1
2	A	1140	ASN	2.1
2	A	749	LEU	2.1
2	A	683	ILE	2.1
2	A	953	ILE	2.1
2	A	1375	CYS	2.1
1	B	283	MET	2.1
2	A	815	VAL	2.1
1	B	369	TYR	2.1
2	A	1629	TYR	2.1
3	C	66	GLN	2.0
1	B	295	GLY	2.0
1	B	549	GLU	2.0
2	A	1610	GLU	2.0
1	B	300	THR	2.0
1	B	371	ILE	2.0
1	B	484	ILE	2.0
2	A	1331	LYS	2.0
2	A	1569	THR	2.0
1	B	406	PRO	2.0
2	A	1672	PHE	2.0
1	B	422	LEU	2.0
2	A	707	ASN	2.0
2	A	1241	ASN	2.0
2	A	1305	LYS	2.0
2	A	814	THR	2.0
2	A	1551	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

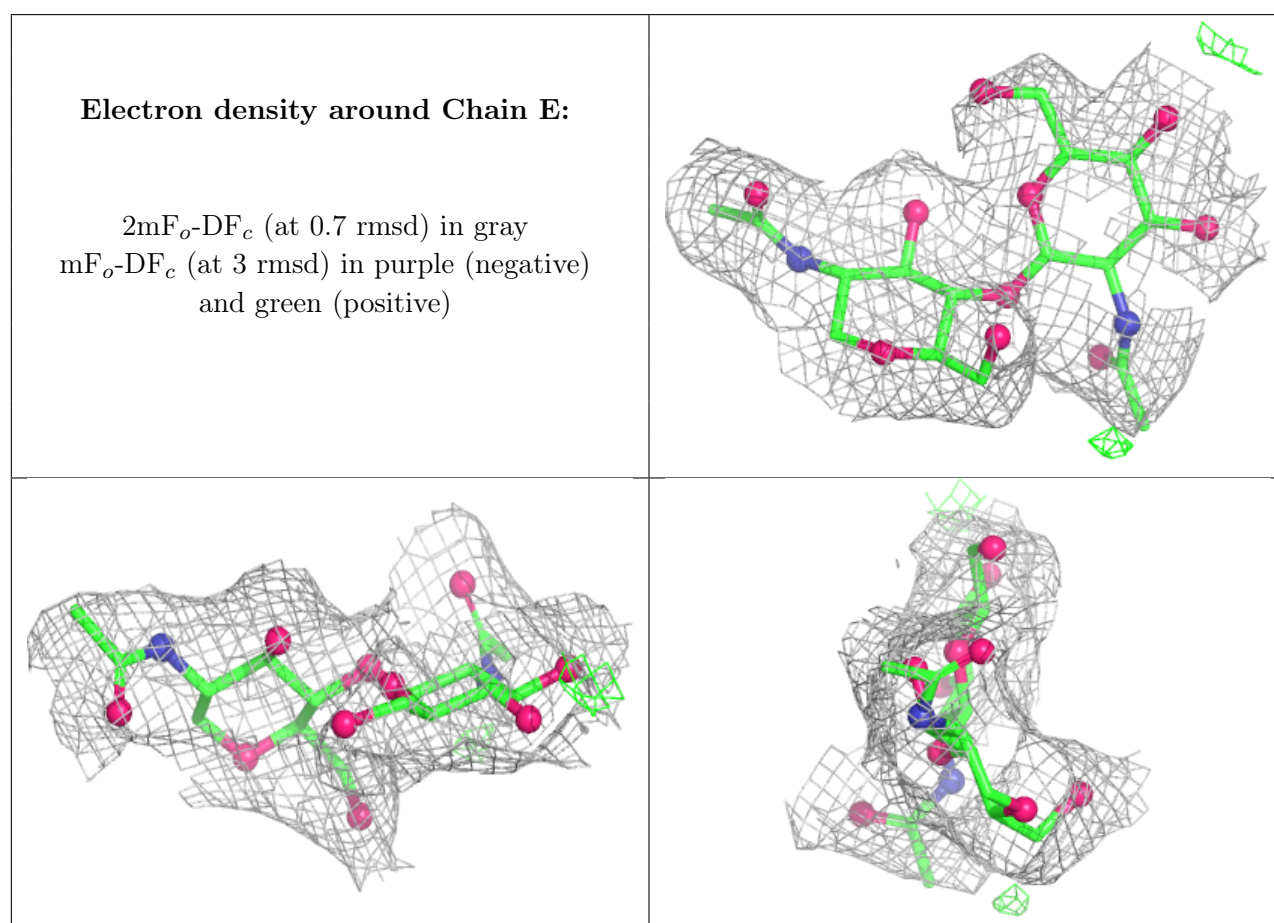
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	E	2	14/15	0.70	0.13	87,90,96,97	0
5	NAG	E	1	14/15	0.92	0.09	51,67,73,82	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	B	702	4/4	0.80	0.23	80,81,82,82	0
7	CYS	A	2006	6/7	0.80	0.24	115,119,124,129	0
6	EDO	A	2004	4/4	0.84	0.19	65,67,68,69	0
6	EDO	A	2005	4/4	0.85	0.27	81,81,83,84	0
6	EDO	D	101	4/4	0.88	0.21	70,73,75,79	0
6	EDO	B	701	4/4	0.90	0.19	88,89,89,90	0
8	DIO	A	2007	6/6	0.90	0.16	73,75,78,79	0
6	EDO	A	2003	4/4	0.91	0.12	40,44,45,51	0
6	EDO	C	201	4/4	0.92	0.14	59,60,60,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.